

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Ashkenazi, Avi J.
Baker, Kevin
Gurney, Austin
Wood, William

10 (ii) TITLE OF INVENTION: Apo-2DcR

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Genentech, Inc.
(B) STREET: 460 Point San Bruno Blvd
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

20 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

30 (vi) CURRENT APPLICATION DATA:

35 (A) APPLICATION NUMBER:
(B) FILING DATE: 18-Jun-1997
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Marschang, Diane L.
(B) REGISTRATION NUMBER: 35,600

(C) REFERENCE/DOCKET NUMBER: P1110

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415/225-5416

5 (B) TELEFAX: 415/952-9881

(C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile Val
1 5 10 15

20 Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg
20 25 30

25 Gln Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg
35 40 45

30 His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser
50 55 60

35 Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr
65 70 75

40 Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val
80 85 90

45 Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg

95 100 105

Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn
110 115 120

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Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu
125 130 135

Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln Cys Val
10 140 145 150

Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr Pro Ala Ala Glu
155 160 165

15 Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
170 175 180

Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
185 190 195

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Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
200 205 210

Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
215 220 225

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Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His Tyr
230 235 240

30 Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile Val Leu Leu
245 250 255

Ile Val Phe Val
259

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 1180 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

15 GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG 50

20 ATTTTTGGGA GTTTGACCAAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC 100

25 CGTTAGGGAA CTCTGGGAC AGAGCGCCCC GGCCGCCTGA TGGCCGAGGC 150

30 AGGGTGCGAC CCAGGACCCA GGACGGCGTC GGGAACCATATA CC ATG 195

Met

1

35 GCC CGG ATC CCC AAG ACC CTA AAG TTC GTC GTC GTC ATC 234

40 Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile

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45 GTC GCG GTC CTG CTG CCA GTC CTA GCT TAC TCT GCC ACC 273

50 Val Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr

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55 ACT GCC CGG CAG GAG GAA GTT CCC CAG CAG ACA GTG GCC 312

60 Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala

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65 CCA CAG CAA CAG AGG CAC AGC TTC AAG GGG GAG GAG TGT 351

70 Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys

45 50

CCA GCA GGA TCT CAT AGA TCA GAA CAT ACT GGA GCC TGT 390
 Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala Cys
 5 55 60 65

AAC CCG TGC ACA GAG GGT GTG GAT TAC ACC AAC GCT TCC 429
 Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser
 10 70 75

AAC AAT GAA CCT TCT TGC TTC CCA TGT ACA GTT TGT AAA 468
 Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys
 80 85 90

TCA GAT CAA AAA CAT AAA AGT TCC TGC ACC ATG ACC AGA 507
 Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg
 15 95 100 105

GAC ACA GTG TGT CAG TGT AAA GAA GGC ACC TTC CGG AAT 546
 Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn
 20 110 115

GAA AAC TCC CCA GAG ATG TGC CGG AAG TGT AGC AGG TGC 585
 Glu Asn Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys
 25 120 125 130

CCT AGT GGG GAA GTC CAA GTC AGT AAT TGT ACG TCC TGG 624
 Pro Ser Gly Glu Val Gln Val Ser Asn Cys Thr Ser Trp
 30 135 140

GAT GAT ATC CAG TGT GTT GAA GAA TTT GGT GCC AAT GCC 663
 Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala
 35 145 150 155

ACT GTG GAA ACC CCA GCT GCT GAA GAG ACA ATG AAC ACC 702

Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr
160 165 170

5 AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG 741
Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met
175 180

AAC ACC AGC CCA GGG ACT CCT GCC CCA GCT GCT GAA GAG 780
Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu
10 185 190 195

ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC CCA GCT GCT 819
Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala
200 205

55 GAA GAG ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC CCA 858
Glu Glu Thr Met Thr Ser Pro Gly Thr Pro Ala Pro
210 215 220

20 GCT GCT GAA GAG ACA ATG ACC ACC AGC CCG GGG ACT CCT 897
Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro
225 230 235

25 GCC TCT TCT CAT TAC CTC TCA TGC ACC ATC GTA GGG ATC 936
Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile
240 245

ATA GTT CTA ATT GTG CTT CTG ATT GTG TTT GTT T 970
Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
30 250 255 259

GAAAGACTTC ACTGTGGAAG AAATTCCCTTC CTTACCTGAA AGGTTCAGGT 1020

AGGCGCTGGC TGAGGGCGGG GGGCGCTGGA CACTCTCTGC CCTGCCTCCC 1070

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TCTGCTGTGT TCCCCACAGAC AGAAACGCC GCCTGCCCAAAAAAAAAA 1120

AAAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1170

5 AAAAAAAAAA 1180

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 299 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly
-40 -35 -30

Asp Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro
-25 -20 -15

Arg Thr Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro
-10 -5 1 5

Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro
10 15 20

Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro
25 30 35

30 Gln Gln Thr Val Ala Pro Gln Gln Arg His Ser Phe Lys Gly
40 45 50

Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala
35 55 60 65

5 Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn
70 75 80

5 Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln
85 90 95

10 Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln
100 105 110

10 Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro Glu Met Cys
115 120 125

15 Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu Val Gln Val Ser Asn
130 135 140

20 Cys Thr Ser Trp Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala
145 150 155

25 Asn Ala Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr
160 165 170

30 Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Asn Thr
175 180 185

35 Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
190 195 200

35 Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
205 210 215

35 Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
220 225 230

35 Ser Pro Gly Thr Pro Ala Ser Ser His Tyr Leu Ser Cys Thr Ile
235 240 245

Val Gly Ile Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
250 255 259

(2) INFORMATION FOR SEQ ID NO:4:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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GCTGTGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG 50

ATTTTTGGGA GTTGACCAAG AG ATG CAA GGG GTG AAG GAG 90
Met Gln Gly Val Lys Glu
-40 -35

CGC TTC CTA CCG TTA GGG AAC TCT GGG GAC AGA GCG CCC 129
Arg Phe Leu Pro Leu Gly Asn Ser Gly Asp Arg Ala Pro
-30 -25

CGG CCG CCT GAT GGC CGA GGC AGG GTG CGA CCC AGG ACC 168
Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro Arg Thr
-20 -15 -10

30 CAG GAC GGC GTC GGG AAC CAT ACC ATG GCC CGG ATC CCC 207
Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro
-5 1 5

35 AAG ACC CTA AAG TTC GTC GTC ATC GTC GCG GTC CTG 246

Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu

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CTG CCA GTC CTA GCT TAC TCT GCC ACC ACT GCC CGG CAG 285
Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln
20 25 30

5 GAG GAA GTT CCC CAG CAG ACA GTG GCC CCA CAG CAA CAG 324
Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln
35 40

10 AGG CAC AGC TTC AAG GGG GAG GAG TGT CCA GCA GGA TCT 363
Arg His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser
45 50 55

15 CAT AGA TCA GAA CAT ACT GGA GCC TGT AAC CCG TGC ACA 402
His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys Thr
60 65 70

20 GAG GGT GTG GAT TAC ACC AAC GCT TCC AAC AAT GAA CCT 441
Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro
75 80

25 TCT TGC TTC CCA TGT ACA GTT TGT AAA TCA GAT CAA AAA 480
Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln Lys
85 90 95

30 CAT AAA AGT TCC TGC ACC ATG ACC AGA GAC ACA GTG TGT 519
His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys
100 105

35 CAG TGT AAA GAA GGC ACC TTC CGG AAT GAA AAC TCC CCA 558
Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro
110 115 120

40 GAG ATG TGC CGG AAG TGT AGC AGG TGC CCT AGT GGG GAA 597
Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu
125 130 135

5 GTC CAA GTC AGT AAT TGT ACG TCC TGG GAT GAT ATC CAG 636
Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln
140 145

10 5 TGT GTT GAA GAA TTT GGT GCC AAT GCC ACT GTG GAA ACC 675
Cys Val Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr
150 155 160

15 CCA GCT GCT GAA GAG ACA ATG AAC ACC AGC CCG GGG ACT 714
Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr
165 170

20 105 CCT GCC CCA GCT GCT GAA GAG ACA ATG AAC ACC AGC CCA 753
Pro Ala Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro
175 180 185

25 150 GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG ACC ACC 792
Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
190 195 200

30 200 AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG 831
Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met
205 210

35 250 ACC ACC AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG 870
Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu
215 220 225

40 300 ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC TCT TCT CAT 909
Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His
230 235

45 350 TAC CTC TCA TGC ACC ATC GTA GGG ATC ATA GTT CTA ATT 948
Tyr Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile
240 245 250

GTG CTT CTG ATT GTG TTT GTT T GAAAGACTTC ACTGTGGAAG 990
Val Leu Leu Ile Val Phe Val
255 259

5 AAATTCCCTTC CTTACCTGAA AGGTTCAGGT AGGCGCTGGC TGAGGGCGGG 1040
GGGCGCTGGA CACTCTCTGC CCTGCCTCCC TCTGCTGTGT TCCCACAGAC 1090
10 AGAAACGCCT GCCCCTGCC CAAAAAAA AAAAAAAA AAAAAAAA 1140
AAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA 1180

(2) INFORMATION FOR SEQ ID NO:5:

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5 CAGGAAACAG CTATGACCAC CTGCACACCT GCAAATCCAT T 41

10 (2) INFORMATION FOR SEQ ID NO:7:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

25 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His
1 5 10 15

30 Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly
20 25 30

35 Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys
30 40 45

40 Gly Cys Arg Lys

49

45 (2) INFORMATION FOR SEQ ID NO:8:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

60 Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn
1 5 10 15

Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln

20

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Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln

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Cys Lys Glu

48

10 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50

GCTAAAGCTG AGGCAGCGGG 70

25 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1799 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

35

CCCACGCGTC CGCATAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT 50

GCGCCCACAA AATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAAC 100

5 CCACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCC ATG GAA 145
Met Glu
1

CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG GCC CGG 184
10 Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
5 10 15

AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC 223
Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala
20 25

AGG CCT GGG CTC CGG GTC CCC AAG ACC CTT GTG CTC GTT 262
Arg Pro Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val
30 35 40

GTC GCC GCG GTC CTG CTG TTG GTC TCA GCT GAG TCT GCT 301
Val Ala Ala Val Leu Leu Leu Val Ser Ala Glu Ser Ala
45 50

25 CTG ATC ACC CAA CAA GAC CTA GCT CCC CAG CAG AGA GCG 340
Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln Gln Arg Ala
55 60 65

30 GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA GAG GGA TTG 379
Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
70 75 80

TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT 418
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp
35 85 90

TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC 457
 Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His
 95 100 105

5 TGG AAT GAC CTC CTT TTC TGC TTG CGC TGC ACC AGG TGT 496
 Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys
 110 115

10 GAT TCA GGT GAA GTG GAG CTA AGT CCC TGC ACC ACG ACC 535
 Asp Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr
 120 125 130

15 AGA AAC ACA GTG TGT CAG TGC GAA GAA GGC ACC TTC CGG 574
 Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe Arg
 135 140 145

20 GAA GAA GAT TCT CCT GAG ATG TGC CGG AAG TGC CGC ACA 613
 Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr
 150 155

25 GGG TGT CCC AGA GGG ATG GTC AAG GTC GGT GAT TGT ACA 652
 Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr
 160 165 170

30 CCC TGG AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC 691
 Pro Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly
 175 180

35 ATC ATC ATA GGA GTC ACA GTT GCA GCC GTA GTC TTG ATT 730
 Ile Ile Ile Gly Val Thr Val Ala Ala Val Val Leu Ile
 185 190 195

GTG GCT GTG TTT GTT TGC AAG TCT TTA CTG TGG AAG AAA 769
 Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys
 200 205 210

15 GTC CTT CCT TAC CTG AAA GGC ATC TGC TCA GGT GGT GGT 808
Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly
215 220

5 225 230 235

10 GGG GCT GAG GAC AAT GTC CTC AAT GAG ATC GTG AGT ATC 886
Gly Ala Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile
240 245

15 250 255 260

20 CAG GAG CCA GCA GAG CCA ACA GGT GTC AAC ATG TTG TCC 964
Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser
265 270 275

25 CCC GGG GAG TCA GAG CAT CTG CTG GAA CCG GCA GAA GCT 1003
Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
280 285

30 GAA AGG TCT CAG AGG AGG AGG CTG CTG GTT CCA GCA AAT 1042
Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn
290 295 300

35 GAA GGT GAT CCC ACT GAG ACT CTG AGA CAG TGC TTC GAT 1081
Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp
305 310

40 GAC TTT GCA GAC TTG GTG CCC TTT GAC TCC TGG GAG CCG 1120
Asp Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro
315 320 325

5 CTC ATG AGG AAG TTG GGC CTC ATG GAC AAT GAG ATA AAG 1159
Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile Lys
330 335 340

5 GTG GCT AAA GCT GAG GCA GCG GGC CAC AGG GAC ACC TTG 1198
Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu
345 350

10 TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG CGA 1237
Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg
355 360 365

15 GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG 1276
Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr
370 375

20 CTG GGA GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC 1315
Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His
380 385 390

25 TTG TTG AGC TCT GGA AAG TTC ATG TAT CTA GAA GGT AAT 1354
Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
395 400 405

30 GCA GAC TCT GCC WTG TCC TAAGTGTG ATTCTCTTCA GGAAGTGAGA 1400
Ala Asp Ser Ala Xaa Ser
410 411

35 CCTTCCCTGG TTTACCTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC 1450
AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC 1500

40 CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACTT TTCACTGCAC 1550

45 TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT 1600

GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTTGGTT TGGGATGTCA 1650

TTGTTTTCAC AGCACTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT 1700

5 TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAG AAAAAAAAAG 1750

GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC 1799

(2) INFORMATION FOR SEQ ID NO:11:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg

1 5 10 15

Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro

20 25 30

Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val

25 40 45

Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp

50 55 60

30 Leu Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser

65 70 75

Pro Ser Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp

80 85 90

35

	Gly Arg Asp Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr		
	95	100	105
	His Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp		
5	110	115	120
	Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Arg Asn Thr		
	125	130	135
10	Val Cys Gln Cys Glu Glu Gly Thr Phe Arg Glu Glu Asp Ser Pro		
	140	145	150
	Glu Met Cys Arg Lys Cys Arg Thr Gly Cys Pro Arg Gly Met Val		
	155	160	165
15	Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val His		
	170	175	180
20	Lys Glu Ser Gly Ile Ile Gly Val Thr Val Ala Ala Val Val		
	185	190	195
25	Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys		
	200	205	210
	Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Asp		
	215	220	225
30	Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp		
	230	235	240
	Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val		
	245	250	255
35	Pro Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly		
	260	265	270

Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro
275 280 285

Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala
5 290 295 300

Asn Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp
305 310 315

10 Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg
320 325 330

Lys Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu
335 340 345

Ala Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp
350 355 360

20 Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp
365 370 375

Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu
380 385 390

25 Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
395 400 405

30 Ala Asp Ser Ala Xaa Ser
410 411

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

35 (B) TYPE: Nucleic Acid

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- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:13:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30